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<110> Sakowicz, Roman
Goldstein, Lawrence S. B.
The Regents of the University of California

<120> Identification and Expression of a Novel Kinesin Motor Protein

<130> 18557C-000710US

<140> US 09/235,416
<141> 1999-01-22

<150> WO PCT/US99/01355
<151> 1999-01-22

<150> US 60/072,361
<151> 1998-01-23

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
<211> 784
<212> PRT
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed microtubule motor protein

<220>
<221> DOMAIN
<222> (1)..(357)
<223> kinesin-like microtubule motor domain

<220>
<221> DOMAIN
<222> (358)..(442)
<223> neck domain links motor domain to stalk domain

<220>
<221> DOMAIN
<222> (443)..(601)
<223> stalk domain, unc-104 family domain

<220>
<221> DOMAIN
<222> (602)..(784)
<223> tail domain

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 35 40 45
 Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe
 50 55 60
 Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg
 65 70 75 80
 Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
 85 90 95
 Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
 100 105 110
 Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
 115 120 125
 Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
 130 135 140
 Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
 145 150 155 160
 Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
 165 170 175
 Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
 180 185 190
 Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
 195 200 205
 Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
 210 215 220
 Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
 225 230 235 240
 Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
 245 250 255
 Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
 260 265 270
 Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
 275 280 285
 Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
 290 295 300
 Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
 305 310 315 320
 Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
 325 330 335
 Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
 340 345 350

Bcont

Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
 355 360 365
 Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
 370 375 380
 Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly
 385 390 395 400
 Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
 405 410 415
 Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
 420 425 430
 Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
 435 440 445
 Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
 450 455 460
 Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
 465 470 475 480
 Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
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 Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
 500 505 510
 Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
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 Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
 530 535 540
 Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
 545 550 555 560
 Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
 565 570 575
 Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
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 His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
 595 600 605
 His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
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 Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
 625 630 635 640
 Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
 645 650 655
 Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
 660 665 670

Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
675 680 685

Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
690 695 700

Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
705 710 715 720

Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
725 730 735

Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
740 745 750

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Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
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<210> 2
<211> 2352
<212> DNA
<213> *Thermomyces lanuginosus*

<220>
<223> TL-gamma ATP-dependent plus end-directed
microtubule motor protein

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cctcgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaa 180
gcatttgcgt tcgacggtc gtattggtcc ttgacaaga atgctcccaa ctatgcgaga 240
caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
tatggcaagg agcatggcgt gatcccgcg atttgccagg acatgttccg gcgtattaat 420
gaactgcaga aggacaagaa cctcacttgc accgtcgaag ttctgtactt ggaaatttac 480
aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
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aaccacgcag tggtaaatga agaccgaac gcgcggatga tccgcgagtt gaaggaggaa 1140
ctcgcgcagc tgaggagcaa actccagagc agtggtggag gtggaggtg tgaggagggt 1200
tctggcgggc cagtggagga atcgtaccgc cccgacacgc cgctcgagaa gcaaatctg 1260
tcgattcagc agccgatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa 1320
ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggaactggg tatcagcatc 1440
gaaaagggtc ttgttggtcc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
gatgatcttc ttctggtgta gtgtcttgc tacaacatca agccggggca gacaagggtt 1560
ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgag cggtacag 1740

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atcatcctgg gcgatttcca catttttcga ttcaaccatc cggaagaagc tcgtgcggaa 1800
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ccaggccgctc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg 1980
gaagctgcta gcgcgacccct agggttggat cagaagatct ctcatctgac agatgacgag 2040
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gacaacgaag atagcgattc gcagagttcg ttcccggtcc gtgacaaata catgtccaat 2160
ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt 2220
gatgacgacg gtgacgcgct gttttttggt gataagaagt cgaaacagga tgcgtctaata 2280
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<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:primer

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<400> 3
atgtcgggcg gtggaaatat c 21

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```

<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:primer

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<400> 4
gaattcctgc ttcgctgttt tca 23

```

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<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:degenerate
forward primer

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<220>
<221> modified_base
<222> (25)
<223> n = a, c, g or t

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<400> 5
gcgcggatcc atytttgcht ayggnacarac 30

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```

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:degenerate
reverse primer

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B'cont

<220>
<221> modified_base
<222> (16)
<223> n = a, c, g or t

<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t

<400> 6
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30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
reverse primer

<220>
<221> modified_base
<222> (16)
<223> n = a, c, g or t

<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t

<400> 7
gcgcgaattc tcdctnccdg cvarrtcac

30

B'